Amendments to the Specification:

Please replace the paragraph (or section) beginning at page 3, line 17, with the following redlined paragraph (or section):

The present invention provides expression vectors and methods for expression heterologous nucleic acid sequences using such expression vectors. Within one embodiment the expression vector comprises an expression cassette comprising from 5' to 3' the following elements: a CMV promoter sequence, a CMV enhancer sequence, a CMV intron A sequence from the CMV major immediate early gene, a heterologous nucleic acid sequence, and a polyadenylation site, wherein the promoter is operably linked to the heterologous nucleic acid sequence. In some embodiments, the CMV intron A sequence has a deletion from about base 1513 to about base 1736. In other embodiments, the heterologous nucleic acid encodes a cancer antigen, such as, for example, L523S (SEQ ID NO:6). In some embodiments the expression cassette comprises ~~nucleotides 54-3675 of the sequence set forth in SEQ ID NO:3,~~ nucleotides 1-1653 of the sequence set forth in SEQ ID NO:3, or the nucleotide sequence set forth in SEQ ID NO:3. The invention also provides host cells comprising the expression vectors described above. In some embodiments, the host cell is *E. coli* or mammalian cells. The invention further provides immunogenic compositions comprising the expression vector described above.

Another embodiment of the invention provides a methods for expressing a heterologous nucleic acid sequence. A host cell comprising an expression vector comprising an expression cassette comprising from 5' to 3' the following elements: a CMV promoter sequence, a CMV enhancer sequence, a CMV intron A sequence from the CMV major immediate early gene, a heterologous nucleic acid sequence, and a polyadenylation site, wherein the promoter is operably linked to the heterologous nucleic acid sequence is cultured. In some embodiments, the CMV intron A sequence has a deletion from about base 1513 to about base 1736. In some embodiments, the heterologous nucleic acid encodes a cancer antigen, such as, for example, L523S (SEQ ID NO:6). In some embodiments, the expression cassette comprises ~~nucleotides 54-3675 of the sequence set forth in SEQ ID NO:3,~~ nucleotides 1-1653 of the sequence set forth in SEQ ID NO:3, or the nucleotide sequence set forth in SEQ ID NO:3. In some embodiments, the

expression cassette comprises the nucleotides set forth in SEQ ID NO:4. In some embodiments, the host cell is *E. coli* or mammalian cells.

Please replace the paragraph (or section) beginning at page 9, line 11, with the following redlined paragraph (or section):

A preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.* (1977) Nuc. Acids Res. 25:3389-3402 and Altschul *et al.* (1990) J. Mol. Biol. 215:403-410, respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (~~http://~~www.ncbi.nlm.nih.gov~~/~~). Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Please replace the paragraph (or section) beginning at page 23, line 9, with the following redlined paragraph (or section):

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used to introduce the expression vector. These include the use of reagents such as ~~Superfect~~ SUPERFECT reagents (Qiagen), liposomes, calcium phosphate transfection, polybrene, protoplast fusion, electroporation, microinjection, plasmid vectors, viral vectors, biolistic particle acceleration (the gene gun), or any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*, *supra*).

Please replace the paragraph (or section) beginning at page 23, line 27, with the following redlined paragraph (or section):

Any of the well known procedures for introducing foreign nucleotide sequences into host cells may be used to introduce the expression vector. These include the use of reagents such as ~~Superfect~~ SUPERFECT reagents (Qiagen), liposomes, calcium phosphate transfection, polybrene, protoplast fusion, electroporation, microinjection, plasmid vectors, viral vectors, biolistic particle acceleration (the gene gun), or any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*, *supra*).

Please replace the paragraph (or section) beginning at page 62, line 8, with the following redlined paragraph (or section):

pCRXA20 is 3584 bases and comprises 5 regions. The first region (bases 1-1368) was cloned from viral DNA of the human CMV virus, Towne strain(ATCC Number: VR-977). This first region contains the viral promoter, enhancer, and intron A, corresponding to bases 512-1513 and 1736-2094 of the major-immediate early gene of CMV (~~Genbank~~ GENBANK Accession No. M60321) and drives the mRNA transcription of a cloned gene. The second region (bases 1369-1416) contains recognition sites for 6 restriction enzymes and was derived from annealed

oligonucleotides. This region allows for cloning of a gene into the vector. The third region (bases 1417-1651) was cloned from bases 3407-3634 of the plasmid pRSVneo (ATCC# 37198). This third region contains the early and late polyadenylation signals of the SV40 virus and provides the necessary polyA sites for the mRNA transcript of a cloned gene. The fourth region (bases 1652-2581) contain a bacterial promoter and the gene for Kanamycin resistance. The promoter was cloned from bases 2463-2600 of the plasmid pUC(ATCC# 37252), and bases 4589-5383 of the gene from pRSVneo. This fourth region allows for the selective growth of bacteria containing the vector. The fifth region (bases 2582-3584) contain an origin of replication, cloned from to bases 605-1600 of pUC and allows for the propagation of the vector in bacteria. ~~Figure 1.~~

Please replace the paragraph (or section) beginning at page 62, line 26, with the following redlined paragraph (or section):

A replication defective E1 and E3 deleted human adenovirus serotype 5 vector expressing human L523S under the control of the CMV promoter was generated using standard molecular biology techniques (~~AdEasy~~ ADEASY System, Johns Hopkins University, Baltimore, MD). The DNA sequence of the L523S-Adenovirus- vector is set forth in SEQ ID NO:5. The cDNA sequence encoding the full-length L523S protein is set forth in SEQ ID NO:6 with the corresponding amino acid sequence set forth in SEQ ID NO:7.